

GenCore version 5.1.9
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OM protein ~ protein search, using sw model

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-Run on: June 10, 2006, 05:36:37 ; Search time 16 Seconds
          (without alignments)
          272.619 Million cell updates/sec

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Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDYFLLCDAEG.....TQECFIPOAKLSPQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: '64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

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Maximum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Local processing: Minimum Match 0%
Maximum Match 100%

Maximum PACC 100%
Listing first 45 summaries

Database : Published Applications AA New: *

1: /EMC_Celerra_SID33/prodata/1/pubpaa/US09_NEW_PUB_pcp.*
2: /EMC_Celerra_SID33/prodata/1/pubpaa/US06_NEW_PUB_pcp.*
3: /EMC_Celerra_SID33/prodata/1/pubpaa/US07_NEW_PUB_pcp.*
4: /EMC_Celerra_SID33/prodata/1/pubpaa/US08_NEW_PUB_pcp.*
5: /EMC_Celerra_SID33/prodata/1/pubpaa/PCT_NEW_PUB_pcp.*
6: /EMC_Celerra_SID33/prodata/1/pubpaa/US11_NEW_PUB_pcp.*
7: /EMC_Celerra_SID33/prodata/1/pubpaa/US11_NEW_PUB_pcp.*
8: /EMC_Celerra_SID33/prodata/1/pubpaa/US60_NEW_PUB_pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	498.5	27.5	403	6	US-10-505-928-203	Sequence 203, App	
2	108.5	6.0	1836	7	US-11-313-450-8	Sequence 8, Appli	
3	102.5	5.6	364	7	US-11-293-697-4612	Sequence 4612, Ap	
4	100	5.5	360	7	US-11-242-111-19	Sequence 19, Appl	
5	97.5	5.4	344	6	US-10-953-349-5324	Sequence 5324, Ap	
6	97.5	5.4	419	6	US-10-953-349-5323	Sequence 5323, Ap	
7	97.5	5.4	513	6	US-10-953-349-5322	Sequence 5322, Ap	
8	97.5	5.4	2005	6	US-10-501-814-3	Sequence 3, Appli	
9	97.5	5.4	2005	7	US-11-263-326-131	Sequence 131, App	
10	97.5	5.4	2005	7	US-11-263-326-132	Sequence 132, App	
11	97.5	5.4	2005	7	US-11-263-326-175	Sequence 175, App	
12	97.5	5.4	2005	7	US-11-263-326-176	Sequence 176, App	
13	97.5	5.4	2005	7	US-11-263-326-177	Sequence 177, App	
14	97.5	5.4	2005	7	US-11-263-326-178	Sequence 178, App	
15	97.5	5.4	2005	7	US-11-263-326-179	Sequence 179, App	
16	97.5	5.4	2005	7	US-11-313-450-4	Sequence 4, Appli	
17	96.5	5.3	2005	7	US-11-263-326-133	Sequence 133, App	
18	96	5.3	1980	7	US-11-263-326-128	Sequence 128, App	
19	96	5.3	1980	7	US-11-263-326-134	Sequence 134, App	
20	96	5.3	1980	7	US-11-313-450-12	Sequence 12, Appl	
21	93.5	5.1	402	6	US-10-471-571A-5294	Sequence 5294, Ap	
22	93.5	5.1	2016	7	US-11-313-450-10	Sequence 10, Appl	
23	92.5	5.1	469	6	US-10-471-571A-5254	Sequence 5254, Ap	
24	92	5.1	2009	7	US-11-263-326-172	Sequence 172, App	
25	91.5	5.0	2006	6	US-11-953-349-38124	Sequence 38124, A	

ALIGNMENTS

RESULT 1

RESULTS I
IIS-10-505-928-203

US-10-503-928-203 : Sequence 203 Application IIS/10505928

; sequence 203, Application US/10
: Publication No US20060088532A1; PUBLICATION NO. US20
: GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

RESEARCHER: DR. JAMES A. HARRIS, JR.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

DATE OF INVENTION: 28967/39178
FILE REFERENCE: 28967/39178

FILE REFERENCE: 2006739178
CURRENT APPLICATION NUMBER: US/10/505.928

; CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 203

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-203

Query Match 27.5%: Score 498 5: DB 6: Length 403:

Best Local Similarity 35.8%
 Best Local Similarity Pred. No. 1.4e-38;
 SCORE 498.3; DB 6
 27.5%;
 Query Match

Score	Local Samirity	95.8%	Recd. NO:	1.7E-30,	
Matches	112:	Conservative	68:	Mismatches	120:
				Indels	13:
				Gaps	7:

QY	12	YFLLCDAAGPWCIIIESAILGIVVTILLALLAFLLMRKIQDCSQNVLPQTQLLFLLSVL	71
Db	45	YVSLCDLDAIMGVVEAVAGALITLLMLTLLVRLPFIKEKEKSPVGLHFLFLGLTL	104
QY	72	GLFGLAFAFIETLNQOTAPVRYFLPGVLFCSCLLAHASNLVKLV- GCVSFSWTTIL	130
Db	105	GLFGTUFAPITQEDETICSVRFLMGVLFCSCLLSQAWRVRLRHGTGPAGW- QLV	163
QY	131	CIAGCSLLQIIIAEYVTLIMTRGMFMVMTPCQLN-VDFVVLLVVVFLMALTFPVSK	189
Db	164	GLALCMLVQVUIAEVWLVLTVLRD----TRPACAYEPMDFVNALIYDMVLLVVTLGLAL	219
QY	190	ATFCGFCENWKQGRLIIFITVLFISIIWVWISMLLRGNPQFORQPDWDPPVCIALVTN	249
Db	220	FTLCCKFKRWKLNGAFLIITAFLSVLIWVWMTVYFGNVKIQGDAMNDPTLAIITLAAS	279
QY	250	AWVFLLLVIVPEL-CILYRSRQCEPCLQGNACPVTAYQHSFQVENQELSRRDSDGA---	305
Db	280	GWVFIHFHAIPEIHCITLLPALQENTPNYFDTSQPMRETAPE-EDVQLPRAYMENKAFSM	338
QY	306	EEDVALTSYGTP	317
Db	339	DEHNAALFTAGFP	351

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OM protein - protein search, using sw model

Run on: June 10, 2006, 05:35:42 ; Search time 178 seconds
(without alignments)
897.804 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIBSTGDFLLCDAEG.....TQECFIPQAKLSPOODAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pdp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pdp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pdp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pdp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pdp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1816	100.0	345	4	US-10-225-567A-619
2	1816	100.0	345	4	US-10-600-816-4
3	1816	100.0	345	5	US-10-500-428-2
4	1816	100.0	345	5	US-10-501-841-56
5	1816	100.0	583	5	US-10-505-486-63
6	1809	99.6	345	4	US-10-467-252-8
7	1797.5	99.0	362	4	US-10-182-822A-14
8	1570.5	86.5	323	4	US-10-343-650A-2
9	1570	86.5	300	4	US-10-467-252-9
10	1570	86.5	317	4	US-10-276-774-2644
11	1318	72.6	300	4	US-10-600-816-5
12	1318	72.6	300	5	US-10-500-428-4
13	1213	66.8	229	4	US-10-029-386-34096
14	727.5	40.1	347	3	US-09-866-050A-326
15	727.5	40.1	357	4	US-10-176-847-60
16	727.5	40.1	357	4	US-10-225-567A-454
17	727.5	40.1	357	4	US-10-224-289-4
18	727.5	40.1	357	4	US-10-295-027-620
19	727.5	40.1	357	4	US-10-600-816-3
20	727.5	40.1	357	4	US-10-600-816-17
21	727.5	40.1	357	4	US-10-600-816-20
22	727.5	40.1	357	4	US-10-600-816-21
23	727.5	40.1	357	5	US-10-935-190-21
24	727.5	40.1	357	5	US-10-936-626-118
25	727.5	40.1	357	5	US-10-936-626-142
26	727.5	40.1	357	5	US-10-938-061-118
27	727.5	40.1	357	5	US-10-938-061-142

28	727.5	40.1	357	5	US-10-510-507-1	Sequence 1, Appli
29	727.5	40.1	357	6	US-11-080-991-60	Sequence 60, Appl
30	727.5	40.1	357	6	US-11-169-041-159	Sequence 159, App
31	727.5	40.1	409	4	US-10-284-049-3009	Sequence 3009, Ap
32	727.5	40.1	595	5	US-10-505-486-94	Sequence 94, Appl
33	726.5	40.0	357	4	US-10-600-816-8	Sequence 8, Appli
34	725.5	40.0	342	4	US-10-224-289-10	Sequence 10, Appl
35	725.5	40.0	357	4	US-10-600-816-9	Sequence 9, Appli
36	723.5	39.8	357	4	US-10-600-816-19	Sequence 19, Appl
37	687.5	37.9	313	3	US-09-864-761-35804	Sequence 35804, A
38	524.5	28.9	400	4	US-10-097-065-146	Sequence 146, App
39	524.5	28.9	400	4	US-10-372-876-146	Sequence 146, App
40	523.5	28.8	401	3	US-09-871-874-11	Sequence 11, Appl
41	523.5	28.8	446	3	US-09-871-874-10	Sequence 10, Appl
42	521.5	28.7	441	3	US-09-871-874-21	Sequence 21, Appl
43	521.5	28.7	441	3	US-09-895-686-1	Sequence 1, Appli
44	521.5	28.7	451	3	US-09-871-874-9	Sequence 9, Appli
45	521.5	28.7	451	3	US-09-871-874-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-225-567A-619
; Sequence 619, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 619
; TYPE: PRT
; LENGTH: 345
; ORGANISM: Homo sapiens
US-10-225-567A-619

Query Match	100.0%	Score 1816;	DB 4;	Length 345;
Best Local Similarity	100.0%	Pred. No. 3.2e-154;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MYKDCIBSTGDFLLCDAEGPWGIIIESLAIGLVVTILLALLAFLLMRKIQDCSQNNVL	60	
Db	1	MYKDCIBSTGDFLLCDAEGPWGIIIESLAIGLVVTILLALLAFLLMRKIQDCSQNNVL	60	
Qy	61	PTOLLFLLSVGLFGAFAPFIELNQOTAPVRVFLGVLFCSCLLAHASNLVKLVRG	120	
Db	61	PTOLLFLLSVGLFGAFAPFIELNQOTAPVRVFLGVLFCSCLLAHASNLVKLVRG	120	
Qy	121	CVSFSWTTILCAIGCSLLQIIATIEYVTLIMTRGMFVNMTPCQLNVDFVLLVYVFL	180	
Db	121	CVSFSWTTILCAIGCSLLQIIATIEYVTLIMTRGMFVNMTPCQLNVDFVLLVYVFL	180	
Qy	181	MALTFPVSKATCGPCENKQGRLLIFITVLSIIIVWVISMILLRGNPQFQPOQDDP	240	
Db	181	MALTFPVSKATCGPCENKQGRLLIFITVLSIIIVWVISMILLRGNPQFQPOQDDP	240	
Qy	241	VVCIALVTWVFLLYIYVPELCILYRSCQECPLQGNACPVYAYOHSFOVENQELSRAR	300	
Db	241	VVCIALVTWVFLLYIYVPELCILYRSCQECPLQGNACPVYAYOHSFOVENQELSRAR	300	
Qy	301	DSGAEEDVALTSYGTPIQPTVDPQECFIPQAKLSPOODAGGV	345	
Db	301	DSGAEEDVALTSYGTPIQPTVDPQECFIPQAKLSPOODAGGV	345	

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OM protein - protein search, using sw model

Run on: June 10, 2006, 05:26:22 ; Search time 296 Seconds
(without alignments)
1078.143 Million cells updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDIESTGDFLLCDABE.....TQECFIPQAKLSPPQAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.2*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	345	1	GPC5D_HUMAN
2	1816	100.0	345	2	Q3KXV3_HUMAN
3	1494	82.3	344	1	GPC5D_MOUSE
4	1494	82.3	344	2	Q3UUY8_MOUSE
5	737.5	40.6	357	2	Q6P25_XENLA
6	727.5	40.1	357	1	RAI3_HUMAN
7	719.5	39.6	357	2	Q3MHQ6_BOVIN
8	700	38.5	356	1	RAI3_MOUSE
9	549.5	30.3	408	2	Q5M7K5_XENTR
10	540	29.7	468	2	Q2YDQ0_BOVIN
11	532.5	29.3	440	1	GPC5C_MOUSE
12	531.5	29.3	457	2	Q3KRC4_RAT
13	523.5	28.8	452	2	Q53GM2_HUMAN
14	521.5	28.7	441	1	GPC5C_HUMAN
15	521.5	28.7	486	2	Q2NL85_HUMAN
16	504	27.8	432	2	Q5M7Q6_XENTR
17	498.5	27.5	403	1	GPC5B_HUMAN
18	497.5	27.4	410	1	GPC5B_MOUSE
19	496.5	27.3	403	2	Q5R3B9_PONPY
20	479.5	26.4	403	2	Q5R6C3_PONPY
21	443	24.4	393	2	Q4RMJ3_TETNG
22	424	23.3	353	2	Q4SGJ6_TETNG
23	398.5	21.9	349	2	Q4S8I2_TETNG
24	341	18.8	537	2	Q4RXZ7_TETNG
25	300.5	16.5	188	2	Q5RK14_RAT
26	260.5	14.3	262	2	Q9JMF0_MOUSE
27	168.5	9.3	893	1	BOSS_DROVI
28	166.5	9.2	1404	2	Q20073_CABEL
29	164.5	9.1	1027	2	Q8J104_SQUAC
30	164	9.0	867	1	GPC6A_BRARE
31	162.5	8.9	896	1	BOSS_DROME

32	162.5	8.9	896	2	Q8MSJ2_DROME
33	162.5	8.9	917	2	Q24265_DROME
34	161.5	8.9	940	2	Q73635_FUGRU
35	159.5	8.8	501	2	Q86UN7_HUMAN
36	159.5	8.8	1078	1	CASR_HUMAN
37	159.5	8.8	1078	2	Q2M1T0_HUMAN
38	158.5	8.7	1085	1	CASR_BOVIN
39	156.5	8.6	581	2	Q4RSV3_MACFA
40	156.5	8.6	1079	1	CASR_MOUSE
41	156.5	8.6	1396	2	Q624E7_CAEBR
42	155	8.5	852	2	Q515C6_9TELE
43	152	8.4	783	2	Q8CDP3_MOUSE
44	151.5	8.3	689	2	Q4T846_TETNG
45	151.5	8.3	877	1	GPC6A_CARAU

ALIGNMENTS

RESULT 1

ID	GPC5D_HUMAN	STANDARD;	PRT;	345 AA.
AC	Q9NZD1; Q725J9; Q8TDS6;			
DT	13-APR-2004, integrated into UniProtKB/Swiss-Prot.			
DT	01-OCT-2000, sequence version 1.			
DT	07-FEB-2006, entry version 26.			
DE	G-protein coupled receptor family C group 5 member D.			
GN	Names=GPC5D;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR			
RP	LOCATION, AND INDUCTION.			
RC	TISSUE=Testis;			
RX	MEDLINE=21210966; PubMed=11311935;			
RA	Braeuner-Osborne H., Jensen A.A., Sheppard P.O., Brodin B.,			
RA	Krogsgaard-Larsen P., O'Hara P.;			
RT	"Cloning and characterization of a human orphan family C G-protein			
RT	coupled receptor GPRC5D.";			
RL	Biochim. Biophys. Acta 1518:237-248 (2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).			
RC	TISSUE=Skin;			
RA	Inoue S., Nanbu T., Shimomura T.;			
RT	"Characterization of GPRC5D, a member of RAIG family in hard			
RT	keratinized structures.";			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 3).			
RX	MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;			
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;			
RT	"Identification of G protein-coupled receptor genes from the human			
RT	genome sequence.";			
RL	FEBS Lett. 520:97-101 (2002).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

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OM protein - protein search, using sw model

Run on: June 10, 2006, 05:29:57 ; Search time 41 Seconds
(without alignments)
809.629 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDYFLCLDAEG.....TOECFIPQAKLSPOQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	168.5	9.3	893	2 A47550	bride of sevenless
2	166.5	9.2	1099	2 T16283	hypothetical prote
3	165.5	9.1	896	2 S26740	gene boss protein
4	162.5	8.9	896	2 A36455	bride of sevenless
5	159.5	8.8	1078	2 A56715	calcium receptor (
6	159.5	8.8	1088	2 B56715	calcium receptor (
7	158.5	8.7	1085	2 S40476	Ca(2+)-sensing rec
8	147	8.1	1079	2 I59362	calcium/polyvalent
9	130	7.2	872	2 JH0561	metabotropic gluta
10	130	7.2	879	2 JH0561	metabotropic gluta
11	130	7.2	879	2 JH0562	metabotropic gluta
12	122	6.7	298	2 S15433	hypothetical prote
13	122	6.7	496	2 E82940	hypothetical prote
14	119	6.6	150	2 S43955	probable NADH2 deh
15	116.5	6.4	826	2 T28858	hypothetical prote
16	111	6.1	678	2 B71308	hypothetical prote
17	110	6.1	281	1 S26018	NADH2 dehydrogenas
18	110	6.1	635	1 A64162	cytochrome c-type
19	109.5	6.0	328	2 T11227	NADH2 dehydrogenas
20	109.5	6.0	1840	1 CHRTM1	sodium channel pro
21	109	6.0	288	2 S36954	cytochrome-c oxida
22	109	6.0	288	2 S36955	cytochrome-c oxida
23	108.5	6.0	1835	2 I54323	sodium channel alp
24	108.5	6.0	1836	2 J64893	sodium channel alp
25	108.5	6.0	1836	2 J50648	sodium channel alp
26	108.5	6.0	1836	2 I51964	sodium channel alp
27	108	5.9	445	2 E22845	hypothetical prote
28	108	5.9	871	2 A46742	metabotropic gluta
29	107.5	5.9	287	2 A25877	cytochrome-c oxida

ALIGNMENTS

RESULT 1

A47550

Bride of sevenless precursor - fruit fly (Drosophila virilis)

N;Alternate names: boss

C;Species: Drosophila virilis

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A47550

R;Hart, A.C.; Harrison, S.D.; Van Vactor Jr., D.L.; Rubin, G.M.; Zipursky, S.L.

Proc. Natl. Acad. Sci. U.S.A. 90, 5047-5051, 1993

A;Title: The interaction of bride of sevenless with sevenless is conserved between Drosophila and Drosophila

A;Reference number: A47550; MUID:93281693; PMID:8506350

A;Accession: A47550

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-893 <HAR>

A;Cross-references: UNIPROT:Q24738; UNIPARC:UPI0000126A67; GB:L08132; NID:G290215; PII

C;Genetics:

A;Gene: FlyBase:Dvir/boss

A;Cross-references: FlyBase:FBgn0013105

A;Introns: 14/3; 175/3; 324/3; 808/3

C;Keywords: transmembrane protein

Query Match 9.3%; Score 168.5; DB 2; Length 893;

Best Local Similarity 21.2%; Pred. No. 3.3e-06;

Matches 84; Conservative 70; Mismatches 116; Indels 127; Gaps 20;

QY 4 DCIESTGD---YFLCLDAEGP--WGIIIE-----SLAILGIVVTILLALLFLMRKI 51

DB 497 NCQFTAGENRRYPFLFDGESVMEFWRIKLDTWATGTLTAAILGLIAT-LAILVFIVRISL 555

QY 52 QDCSQNVLPQTQLFLSLVLGLAFATIE-----LNQQTAPVRYP 94

DB 556 GDVFEGNPV-TSILLLLSLVFCSEVPEFMEYVGEQNSHVTFEDVHTLN-TLCGVRF 613

QY 95 LFGVLFCALCFSCLLAHASNLVKL-----VRGCVSFSWTILC-----IAIGCSLLQ 140

DB 614 IMTLVCFVFSLLLCRAVMLASIGSEGGFLSHVNGYIQ-----AIICVLSVFVQVMSVOL 669

QY 141 III---ATEYVTLIMTRGMFMVMTPCQ-----LNVDVFLVLLVFLFMALTF 186

DB 670 LVVMHLASSVS-----CENIYVGRWLGLAYDFLL-----CSLVSVPF 711

QY 187 VSKATPCGCENKQGRILFIVTLPESIIIVVWISMLLRGNPQFORQPDQVPCIAL 246

DB 712 IYRSQ-----RNRYE-GILIVGAVLLIISVIALSMFGD-----EWRDAAIPLGM 758

QY 247 VTNANVFLLYIVPELCILYRSCRCPCLOGNACPTAYQHSFOVENQELSRARDGAE 306

DB 759 QASGAVLVGIIIPRTFLIVRG-----IERSDIAQALPS--- 792

QY 307 EDVALTS--YGTPIQPTVDPTQECFIPQAKLSPOOD 341

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 05:26:07 ; Search time 199 Seconds
(without alignments)
792.662 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIBSTGDFYLLCDAEG.....TOECFIPQAKLSPOQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	1816	100.0	345	Abp81722 Human G p
2	1816	100.0	345	Abd80899 Anorexia
3	1816	100.0	345	Ad67579 Human Ly1
4	1816	100.0	345	Ado29466 Human GPC
5	1816	100.0	583	Adf70440 Orphan re
6	1809	99.6	345	Ab71329 Human GCR
7	1804	99.3	345	Ad810857 Human the
8	1797.5	99.0	362	Aae06764 Human G-p
9	1570.5	86.5	323	Ab69174 Human G-p
10	1570.5	86.5	323	Abp95596 Human GPC
11	1570	86.5	300	Ab71330 Human GCR
12	1570	86.5	300	Adc98222 Human G p
13	1570	86.5	317	Abb12274 Human orp
14	1570	86.5	317	Ad812107 Human the
15	1318	72.6	300	Ad80901 Anorexia
16	1318	72.6	300	Adc98220 Mouse G p
17	1318	72.6	300	Ado29467 Mouse GPC
18	1213	66.8	229	Ab60462 Human gen
19	727.5	40.1	347	Aay76071 Rat skin
20	727.5	40.1	347	Ab56010 Skin cell
21	727.5	40.1	347	Abb72210 Human pro
22	727.5	40.1	352	Adi28547 Human GPC
23	727.5	40.1	352	Adi28461 Human GPC

24	727.5	40.1	357	4	AAB68891	Aab68891 Human REC
25	727.5	40.1	357	4	AAB93311	Aab93311 Human pro
26	727.5	40.1	357	6	ABR58569	AbR58569 Human can
27	727.5	40.1	357	6	ABJ37054	Abj37054 Human bre
28	727.5	40.1	357	6	ABR42649	AbR42649 Human GPC
29	727.5	40.1	357	6	ABP81984	Abp81984 Human G p
30	727.5	40.1	357	7	ADD93239	AdD93239 RAIG1. 1/
31	727.5	40.1	357	7	ADN39302	AdN39302 Cancer/an
32	727.5	40.1	357	8	ADI28460	Adi28460 Human GPC
33	727.5	40.1	357	8	ADO29632	Ado29632 Human GPC
34	727.5	40.1	357	8	ADR48222	AdR48222 Human ret
35	727.5	40.1	357	8	ABMB1354	AbmB1354 Tumour-as
36	727.5	40.1	357	8	ADU06613	Adu06613 Novel bro
37	727.5	40.1	357	9	AEA00166	Aea00166 Human TAT
38	727.5	40.1	357	9	AEA00190	Aea00190 Human TAT
39	727.5	40.1	357	9	AEA00686	Aea00686 Human TAT
40	727.5	40.1	357	9	AEA00710	Aea00710 Human TAT
41	727.5	40.1	357	9	AED47479	Aed47479 Retinoic
42	727.5	40.1	401	8	ADX97565	Adx97565 Pancreat
43	727.5	40.1	409	5	ABP41877	Abp41877 Human ova
44	727.5	40.1	595	7	ADF70471	Adf70471 Orphan re
45	726.5	40.0	357	8	ADI28535	Adi28535 Human GPC

ALIGNMENTS

RESULT 1

ABP81722
ID ABP81722 standard; protein; 345 AA.

XX AC ABP81722;

XX DT 04-MAR-2003 (first entry)

XX DE Human G protein-coupled receptor GPCR5D protein SEQ ID NO:619.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burmer GC, Roush CL, Brown JP;

XX XX WPI; 2003-046718/04.

XX DR N-PSDB; ABZ42568.

XX XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

XX PS Disclosure; Fig 1; 523pp; English.